



RAW SEQUENCE LISTING

DATE: 11/26/2003

PATENT APPLICATION: US/09/243,008

TIME: 15:04:13

Input Set : N:\Crf3\RULE60\09243008.RAW.txt

Output Set: N:\CRF4\11262003\I243008.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Seed, Brian et al.

7 (ii) TITLE OF INVENTION: Redirection of Cellular Immunity by

8 Receptor Chimeras

10 (iii) NUMBER OF SEQUENCES: 40

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Fish & Richardson P.C.

14 (B) STREET: 225 Franklin Street

15 (C) CITY: Boston

16 (D) STATE: MA

17 (E) COUNTRY: USA

18 (F) ZIP: 02110-2804

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

22 (B) COMPUTER: IBM PS/2 Model 50Z or 55SX

23 (C) OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

24 (D) SOFTWARE: Wordperfect (Version 5.0)

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/243,008

C--> 28 (B) FILING DATE: 02-Feb-1999

41 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/08/394,176

32 (B) FILING DATE: SEPTEMBER 11, 1995

34 (A) APPLICATION NUMBER: 08/203,866

35 (B) FILING DATE: February 28, 1994

38 (A) APPLICATION NUMBER: 07/847,566

39 (B) FILING DATE: March 6, 1992

42 (A) APPLICATION NUMBER: 07/665,961

43 (B) FILING DATE: March 7, 1991

45 (viii) ATTORNEY/AGENT INFORMATION:

46 (A) NAME: Karen F. Lech, Ph.D

47 (B) REGISTRATION NUMBER: 35,238

48 (C) REFERENCE/DOCKET NUMBER: 00786/270001

50 (ix) TELECOMMUNICATION INFORMATION:

51 (A) TELEPHONE: (617) 542-5070

52 (B) TELEFAX: (617) 542-8906

53 (C) TELEX: 200154

56 (2) INFORMATION FOR SEQ ID NO: 1:

58 (i) SEQUENCE CHARACTERISTICS:

59 (A) LENGTH: 1728 base pairs

60 (B) TYPE: nucleic acid

61 (C) STRANDEDNESS: double

ENTERED

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62      (D) TOPOLOGY: linear
64      (ii) MOLECULE TYPE: DNA (genomic)
66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68      ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC TGCAACTGGC      50
70      GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG GGCAAAAAAG      100
72      GGGATACAGT GGAAGTACC TGTACAGCTT CCCAGAAGAA GAGCATACAA      150
74      TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA ATCAGGGCTC      200
76      CTTCTTAAGT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT GACTCAAGAA      250
78      GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA GAATCTTAAG      300
80      ATAGAAGATC CAGATACTTA CATCTGTGAA GTGGAGGACC AGAAGGAGGA      350
82      GGTGCAATTG CTAGTGTTCG GATTGACTGC CAACTCTGAC ACCCACCTGC      400
84      TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC TGGTAGTAGC      450
86      CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC AGGGGGGGAA      500
88      GACCCCTCTC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC ACCTGGACAT      550
90      GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAT AGACATCGTG      600
92      GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA AAGAGGGGGA      650
94      ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA AAGCTGACGG      700
96      GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC CTCCAAGTCT      750
98      TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA AACGGGTAC      800
100     CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC CACCTCACCC      850
102     TGCCCCAGGC CTTGCCCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC      900
104     CTTGAAGCGA AAACAGGAAA GTTGCATCAG GAAGTGAACC TGGTGGTGAT      950
106     GAGAGCCACT CAGCTCCAGA AAAATTGAC CTGTGAGGTG TGGGGACCCA      1000
108     CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA GGAGGCAAAG      1050
110     GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT      1100
112     GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCTTGCTG GAATCCAACA      1150
114     TCAAGGTTCT GCCACATGG TCCACCCCGG TGCACGCGGA TCCCAAACCTC      1200
116     TGCTACTTGC TGATGGAAT CCTCTTCATC TACGGAGTCA TCATCACAGC      1250
118     CCTGTACCTG AGAGCAAAT TCAGCAGGAG TGCAGAGACT GCTGCCAACC      1300
120     TGCAGGACCC CAACCAGCTC TACAATGAGC TCAATCTAGG GCGAAGAGAG      1350
122     GAATATGACG TCTTGGAGAA GAAGCGGGCT CGGGATCCAG AGATGGGAGG      1400
124     CAAACAGCAG AGGAGGAGGA ACCCCCAGGA AGGCGTATAC AATGCACTGC      1450
126     AGAAAGACAA GATGCCAGAA GCCTACAGTG AGATCGGCAC AAAAGGCGAG      1500
128     AGGCGGAGAG GCAAGGGGCA CGATGGCCTT TACCAGGACA GCCACTTCCA      1550
130     AGCAGTGCAG TTCGGAACA GAAGAGAGAG AGAAGGTTCA GAACTCACAA      1600
132     GGACCCCTTG GTTAAGAGCC CGCCCCAAG GTGAAAGCAC CCAGCAGAGT      1650
134     AGCCAATCCT GTGCCAGCGT CTTCAGCATC CCCACTCTGT GGAGTCCATG      1700
136     GCCACCCAGT AGCAGCTCCC AGCTCTAA      1728
139 (2) INFORMATION FOR SEQ ID NO: 2:
141     (i) SEQUENCE CHARACTERISTICS:
142         (A) LENGTH: 1389 base pairs
143         (B) TYPE: nucleic acid
144         (C) STRANDEDNESS: double
145         (D) TOPOLOGY: linear
147     (ii) MOLECULE TYPE: DNA (genomic)
149     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
152     ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC TGCAACTGGC      50
154     GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG GGCAAAAAAG      100
156     GGGATACAGT GGAAGTACC TGTACAGCTT CCCAGAAGAA GAGCATACAA      150

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158	TTCCA	CTGGA	AAA	ACTCCAA	CCAGATAAAAG	ATTCTGGGAA	ATCAGGGGCTC	200
160	CTTCTTAACT	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	GA	CTCAAGAA	250	
162	GAAGCCTTTG	GGACCAAGGA	AACTTCCCCC	TGATCATCAA	GAATCTTAAG	300		
164	ATAGAAGACT	CAGATACTTA	CATCTGTGAA	GTGGAGGACC	AGAAGGAGGA	350		
166	GGTGCAATTG	CTAGTGTTTCG	GATTGACTGC	CAACTCTGAC	ACCCACCTGC	400		
168	TTCAGGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCC	TGGTAGTAGC	450		
170	CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAACATAC	AGGGGGGGAA	500		
172	GACCCTCTCC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	ACCTGGACAT	550		
174	GCACTGTCTT	GCAGAACCAG	AAGAAGGTGG	AGTTCAAAAT	AGACATCGTG	600		
176	GTGCTAGCTT	TCCAGAAGGC	CTCCAGCATA	GTCTATAAGA	AAGAGGGGGA	650		
178	ACAGGTGGAG	TTCTCCTTCC	CACTCGCCTT	TACAGTTGAA	AAGCTGACGG	700		
180	GCAGTGGCGA	GCTGTGGTGG	CAGGCGGAGA	GGGCTTCCTC	CTCCAAGTCT	750		
182	TGGATCACCT	TTGACCTGAA	GAACAAGGAA	GTGTCTGTAA	AACGGGTTAC	800		
184	CCAGGACCCT	AAGCTCCAGA	TGGGCAAGAA	GCTCCCGCTC	CACCTCACCC	850		
186	TGCCCCAGGC	CTTGCCTCAG	TATGCTGGCT	CTGGAACCT	CACCCTGGCC	900		
188	CTTGAAGCGA	AAACAGGAAA	GTTGCATCAG	GAAGTGAACC	TGGTGGTGAT	950		
190	GAGAGCCACT	CAGCTCCAGA	AAAATTTGAC	CTGTGAGGTG	TGGGGACCCA	1000		
192	CCTCCCCTAA	GCTGATGCTG	AGCTTGAAAC	TGGAGAACAA	GGAGGCAAAG	1050		
194	GTCTCGAAGC	GGGAGAAGCC	GGTGTGGGTG	CTGAACCCCTG	AGGCGGGGAT	1100		
196	GTGGCAGTGT	CTGCTGAGTG	ACTCGGGACA	GGTCTGTGCTG	GAATCCAACA	1150		
198	TCAAGGTTCT	CCCCACATGG	TCCACCCCGG	TGCACGCGGA	TCCGCAGCTC	1200		
200	TGCTATATCC	TGGATGCCAT	CCTGTTTTTG	TATGGTATTG	TCCTTACCCT	1250		
202	GCTCTACTGT	CGACTCAAGA	TCCAGGTCCG	AAAGGCAGAC	ATAGCCAGCC	1300		
204	GTGAGAAATC	AGATGCTGTC	TACACGGGCC	TGAACACCCG	GAACCAGGAG	1350		
206	ACATATGAGA	CTCTGAAACA	TGAGAAACCA	CCCCAATAG		1389		
209	(2) INFORMATION FOR SEQ ID NO: 3:							
211	(i) SEQUENCE CHARACTERISTICS:							
212	(A) LENGTH: 1599 base pairs							
213	(B) TYPE: nucleic acid							
214	(C) STRANDEDNESS: double							
215	(D) TOPOLOGY: linear							
217	(ii) MOLECULE TYPE: DNA (genomic)							
219	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:							
222	ATGAACCGGG	GAGTCCCTTT	TAGGCACTTG	CTTCTGGTGC	TGCAACTGGC	50		
224	GCTCCTCCCA	GCAGCCACTC	AGGGAAACAA	AGTGGTGCTG	GGCAAAAAAG	100		
226	GGGATACAGT	GGA	ACTGACC	TGTACAGCTT	CCCAGAAGAA	GAGCATACAA	150	
228	TTCCA	CTGGA	AAA	ACTCCAA	CCAGATAAAAG	ATTCTGGGAA	ATCAGGGGCTC	200
230	CTTCTTAACT	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	GA	CTCAAGAA	250	
232	GAAGCCTTTG	GGACCAAGGA	AACTTCCCCC	TGATCATCAA	GAATCTTAAG	300		
234	ATAGAAGACT	CAGATACTTA	CATCTGTGAA	GTGGAGGACC	AGAAGGAGGA	350		
236	GGTGCAATTG	CTAGTGTTTCG	GATTGACTGC	CAACTCTGAC	ACCCACCTGC	400		
238	TTCAGGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCC	TGGTAGTAGC	450		
240	CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAACATAC	AGGGGGGGAA	500		
242	GACCCTCTCC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	ACCTGGACAT	550		
244	GCACTGTCTT	GCAGAACCAG	AAGAAGGTGG	AGTTCAAAAT	AGACATCGTG	600		
246	GTGCTAGCTT	TCCAGAAGGC	CTCCAGCATA	GTCTATAAGA	AAGAGGGGGA	650		
248	ACAGGTGGAG	TTCTCCTTCC	CACTCGCCTT	TACAGTTGAA	AAGCTGACGG	700		
250	GCAGTGGCGA	GCTGTGGTGG	CAGGCGGAGA	GGGCTTCCTC	CTCCAAGTCT	750		
252	TGGATCACCT	TTGACCTGAA	GAACAAGGAA	GTGTCTGTAA	AACGGGTTAC	800		

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254	CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC CACCTCACCC	850
256	TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC	900
258	CTTGAAGCGA AAACAGGAAA GTTGCATCAG GAAGTGAACC TGGTGGTGAT	950
260	GAGAGCCACT CAGCTCCAGA AAAATTTGAC CTGTGAGGTG TGGGGACCCA	1000
262	CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA GGAGGCAAAG	1050
264	GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT	1100
266	GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCCTGCTG GAATCCAACA	1150
268	TCAAGGTTCT GCCACATGG TCCACCCCGG TGCACGCGGA TCCCAAATC	1200
270	TGCTACCTG TGGATGGAAT CCTCTTCATC TATGGTGTCA TTCTCACTGC	1250
272	CTTGTTCCTG AGAGTGAAGT TCAGCAGGAG CGCAGAGCCC CCCGCGTACC	1300
274	AGCAGGCCCA GAACCAGCTC TATAACGAGC TCAATCTAGG ACGAAGAGAG	1350
276	GAGTACGATG TTTTGGACAA GAGACGTGGC CGGGACCCTG AGATGGGGGG	1400
278	AAAGCCGAGA AGGAAGAACC CTCAGGAAGG CCTGTACAAT GAACTGCAGA	1450
280	AAGATAAGAT GGCGGAGGCC TACAGTGAGA TTGGGATGAA AGGCGAGCGC	1500
282	CGGAGGGGCA AGGGGCACGA TGGCCTTTAC CAGGGTCTCA GTACAGCCAC	1550
284	CAAGGACACC TACGACGCC TTCACATGCA GGCCCTGCCC CCTCGCTAA	1599

287 (2) INFORMATION FOR SEQ ID NO: 4:

289 (i) SEQUENCE CHARACTERISTICS:

290 (A) LENGTH: 575 amino acids

291 (B) TYPE: amino acid

292 (D) TOPOLOGY: linear

294 (ii) MOLECULE TYPE: protein

296 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

298	Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Val	Leu	Gln	Leu
299	1				5					10				15	
300	Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Asn	Lys	Val	Val	Leu	Gly
301				20				25					30		Lys
302	Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys
303			35					40					45		Ser
304	Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly
305		50					55					60			Asn
306	Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg
307	65					70					75				80
308	Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile
309					85					90					95
310	Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val
311				100					105				110		Glu
312	Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala
313			115					120					125		Asn
314	Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu
315		130					135					140			Glu
316	Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg
317	145					150					155				Gly
318	Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu
319				165					170						175
320	Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys
321				180					185					190	Lys
322	Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala
323			195					200					205		Ser

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324 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
325      210      215      220
326 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
327 225      230      235      240
328 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
329      245      250      255
330 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
331      260      265      270
332 Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
333      275      280      285
334 Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
335      290      295      300
336 Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
337 305      310      315      320
338 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
339      325      330      335
340 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
341      340      345      350
342 Lys Arg Glu Lys Pro Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
343      355      360      365
344 Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
345      370      375      380
346 Lys Val Leu Pro Thr Trp Ser Thr Pro Val His Ala Asp Pro Lys Leu
347 385      390      395      400
348 Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Ile Thr
349      405      410      415
350 Ala Leu Tyr Leu Arg Ala Lys Phe Ser Arg Ser Ala Glu Thr Ala Ala
351      420      425      430
352 Asn Leu Gln Asp Pro Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
353      435      440      445
354 Arg Glu Glu Tyr Asp Val Leu Glu Lys Lys Arg Ala Arg Asp Pro Glu
355      450      455      460
356 Met Gly Gly Lys Gln Gln Arg Arg Arg Asn Pro Gln Glu Gly Val Tyr
357 465      470      475      480
358 Asn Ala Leu Gln Lys Asp Lys Met Pro Glu Ala Tyr Ser Glu Ile Gly
359      485      490      495
360 Thr Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
361      500      505      510
362 Asp Ser His Phe Gln Ala Val Gln Phe Gly Asn Arg Arg Glu Arg Glu
363      515      520      525
364 Gly Ser Glu Leu Thr Arg Thr Leu Gly Leu Arg Ala Arg Pro Lys Gly
365      530      535      540
366 Glu Ser Thr Gln Gln Ser Ser Gln Ser Cys Ala Ser Val Phe Ser Ile
367 545      550      555      560
368 Pro Thr Leu Trp Ser Pro Trp Pro Pro Ser Ser Ser Ser Gln Leu
369      565      570      575
372 (2) INFORMATION FOR SEQ ID NO: 5:
374      (i) SEQUENCE CHARACTERISTICS:
375          (A) LENGTH: 462 amino acids

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VERIFICATION SUMMARY

DATE: 11/26/2003

PATENT APPLICATION: US/09/243,008

TIME: 15:04:14

Input Set : N:\Crf3\RULE60\09243008.RAW.txt

Output Set: N:\CRF4\11262003\I243008.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:532 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:548 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:564 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:581 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:597 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:613 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:629 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:645 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:661 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:677 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:693 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:709 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:725 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:740 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:756 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:772 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:788 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:803 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:839 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:877 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:919 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27